

GenCore version 5.1.6
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OMnucleic - nucleic search, using sw model

Run on: December 9, 2003, 14:17:59 ; Search time 2795 Seconds
(without alignments)
6410.882 Million cell updates/sec

Title: US-09-787-216A-2
Perfect score: 438
Sequence: 1 gtgcacctgactcctgagga.....ccctggcccaagatcac 438

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Result No.	Score	Match	Length	ID	Description
1	428.4	97.8	438	A01592	A01592 Human haemo
2	428.4	97.8	438	AR050456	AR050456 Sequence
3	428.4	97.8	438	AR124584	AR124584 Sequence
4	428.4	97.8	438	AR142760	AR142760 Sequence
5	428.4	97.8	438	I27203	I27203 Sequence 4
6	428.4	97.8	438	I63086	I63086 Sequence 4
7	426.8	97.4	438	A78805	A78805 Sequence 3
8	426.8	97.4	562	AF117710	AF117710 Homo sapi
9	426.8	97.4	658	BC007075	BC007075 Homo sapi
10	425.2	97.1	438	AR030837	AR030837 Sequence
11	425.2	97.1	534	AY136510	AY136510 Homo sapi
12	425.2	97.1	579	AF181989	AF181989 Homo sapi
13	425.2	97.1	581	AF349114	AF349114 Homo sapi
14	425.2	97.1	626	HSBGL1	V00497 Human messe
15	423.6	96.7	444	AR062963	AR062963 Sequence
16	423.6	96.7	544	A18171	A18171 Beta globin
17	423.6	96.7	743	AR228705	AR228705 Sequence
18	422	96.3	549	HSBGLX	V00500 Human messe
19	422	96.3	1140	AR257263	AR257263 Sequence
20	422	96.3	1140	AR257265	AR257265 Sequence
21	421.4	96.2	576	HUMHEMOB	M25113 Human sickl
22	420.4	96.0	743	AR032231	AR032231 Sequence
23	420.4	96.0	743	BD011603	BD011603 Recombina
24	420.4	96.0	743	BD165862	BD165862 Transgeni
25	420.4	96.0	743	I32884	I32884 Sequence 9
26	393.2	89.8	468	AX336431	AX336431 Sequence
27	393.2	89.8	468	AX409658	AX409658 Sequence
28	393.2	89.8	468	HUMBTGLA	M25079 Human sickl
29	377.8	86.3	790	AY034468	AY034468 Homo sapi
30	376.8	86.0	475	AX400061	AX400061 Sequence
31	376	85.8	488	AF181832	AF181832 Homo sapi
32	374.6	85.5	438	AR050454	AR050454 Sequence
33	374.6	85.5	438	AR124582	AR124582 Sequence
34	353.2	80.6	589	OCBGL2	V00879 Messenger R
35	353.2	80.6	589	RABHBA	M10843 Rabbit beta
36	353.2	80.6	589	AX419806	AX419806 Sequence
37	350.4	80.0	454	BD025503	BD025503 Sequence
38	347.2	79.3	498	AX448896	AX448896 Sequence
39	340.4	77.7	438	MIRMRAB	M73997 Mirounga an
40	310	70.8	577	RATHBEM	M17084 Rat major b
41	310	70.8	620	RNBGLOB	X16417 Rat mRNA fo
42	305.2	69.7	441	AB020013	AB020013 Mus muscu
43	305.2	69.7	441	AB020015	AB020015 Mus muscu
44	305.2	69.7	441	AB020017	AB020017 Mus muscu
45	305.2	69.7	444	AF149782	AF149782 Mus muscu

ALIGNMENTS

RESULT 1

A01592
LOCUS A01592 438 bp DNA linear PAT 08-MAR-1993
DEFINITION Human haemoglobin A beta chain.

ACCESSION A01592
VERSION A01592.1 GI:344421

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
1 (bases 1 to 438)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Pred. No. is the number of results predicted by chance to have a

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OM nucleic - nucleic search, using sw model

Run on: December 9, 2003, 14:24:09 ; Search time 2635 Seconds
(without alignments)
4039.985 Million cell updates/sec

Title: US-09-787-216A-2
Perfect score: 438
Sequence: 1 gtgcactgactctgagga.....ccctggcccaagaatcac 438

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	428.4	97.8	508	12	BM263008
2	428.4	97.8	515	13	BU658312
3	428.4	97.8	522	13	BU660954
4	428.4	97.8	566	12	BM690339

C	5	428.4	97.8	572	12	BM142584
	6	428.4	97.8	573	12	BG943930
	7	428.4	97.8	580	13	BU65464
	8	428.4	97.8	588	12	BI909771
C	9	428.4	97.8	590	12	BM091317
C	10	428.4	97.8	591	12	BM090889
C	11	428.4	97.8	591	12	BQ029722
	12	428.4	97.8	593	13	BU664237
C	13	428.4	97.8	595	12	BM994174
	14	428.4	97.8	598	13	BU661951
	15	428.4	97.8	598	14	CB270453
	16	428.4	97.8	601	10	BG534450
	17	428.4	97.8	601	10	AW950603
	18	428.4	97.8	601	14	CD107933
	19	428.4	97.8	603	9	AV722370
C	20	428.4	97.8	605	12	BM662991
C	21	428.4	97.8	606	12	BM992829
C	22	428.4	97.8	607	13	BQ447183
C	23	428.4	97.8	608	13	BU683550
C	24	428.4	97.8	608	14	CA427861
	25	428.4	97.8	609	12	BM597046
C	26	428.4	97.8	609	13	BU682597
	27	428.4	97.8	611	13	BU073853
	28	428.4	97.8	615	12	BM613468
C	29	428.4	97.8	617	13	BU617711
C	30	428.4	97.8	619	12	BM993095
C	31	428.4	97.8	623	14	CA435390
	32	428.4	97.8	626	13	BU662685
	33	428.4	97.8	626	14	CD559383
C	34	428.4	97.8	628	12	BM992554
	35	428.4	97.8	628	13	BU662291
	36	428.4	97.8	628	14	CD108766
C	37	428.4	97.8	629	12	BM992721
C	38	428.4	97.8	629	13	BU617931
	39	428.4	97.8	629	14	CD522665
C	40	428.4	97.8	630	12	BM664514
C	41	428.4	97.8	630	13	BU626306
	42	428.4	97.8	630	14	CD520923
	43	428.4	97.8	630	14	CD559221
C	44	428.4	97.8	631	14	CA427969
C	45	428.4	97.8	632	14	CA425145

ALIGNMENTS

RESULT 1	BM263008	508 bp	mRNA	linear	EST 18-DEC-2001
LOCUS	ig25c03.y1	Human Fetal Pancreas	1B	Homo sapiens	cDNA 5' similar to
DEFINITION	SW:HBB_HUMAN P02023	HEMOGLOBIN BETA CHAIN.	[3]	SW:HBB_HUMAN	
	TR:Q14510	;	mRNA sequence.		
ACCESSION	BM263008				
VERSION	BM263008.1	GI:17926048			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 508)			
AUTHORS	Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.				
	Endocrine Pancreas Consortium				
TITLE	Unpublished				
JOURNAL	Other ESTs: ig25c03.x1				
COMMENT	Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue				
	Endocrine Pancreas Consortium				
	Harvard University, Howard Hughes Medical Institute				
	Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,				

MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmeltont@biohpc.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@imgate.wustl.edu)
Putative full length read
vector to vector length is
Seq primer: -40RP from Gibco
High quality sequence stop: 476.

FEATURES

Location/Qualifiers
1..508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Fetal Pancreas (4 Pooled Donors, 18 - 20 weeks, Stratagene #738023)"
/dev_stage="Fetal Pancreas"
/clone_lib="Human Fetal Pancreas 1B"
/note="Vector: pBluescript SK(-); Site 1: NotI; Site 2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110 E-mail: hinoue@imgate.wustl.edu Tel: 314-362-1916, Fax: 314-747-2692."

BASE COUNT 96 a 135 c 147 g 130 t

Query Match 97.8%; Score 428.4; DB 12; Length 508;
Best Local Similarity 98.6%; Pred. No. 5.2e-103;
Matches 432; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GTGCACCTGACTCCTGAGGAGAGTGGCGCTTACTGCCCTGTGGGCAAGTGAACGTG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
15 GTGCACCTGACTCCTGAGGAGAGTCTGCCGTACTGCCCTGTGGGCAAGTGAACGTG 74
QY 61 GATGAAGTTGGTGGTGGCCCTGGGAGGCTGCTGGTGCTACCTTGACCCAGAGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
75 GATGAAGTTGGTGGTGGCCCTGGGAGGCTGCTGGTGCTACCTTGACCCAGAGG 134
QY 121 TTCTTTGAGTCCTTTGGGATCTGTCCACTCCTGATGCTGTATGGCAACCTAAGGTG 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
135 TTCTTTGAGTCCTTTGGGATCTGTCCACTCCTGATGCTGTATGGCAACCTAAGGTG 194
QY 181 AAGGCTCATGGCAAGAAAGTGTCTGGTGCCTTTAGTGTATGGCTGCTCAGTGGACAAC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
195 AAGGCTCATGGCAAGAAAGTGTCTGGTGCCTTTAGTGTATGGCTGCTCAGTGGACAAC 254
QY 241 CTCAAGGGCACCTTTGCCACACTGAGTGAAGTGCATGCTGCAAGCTGCACGTGGATCCT 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
255 CTCAAGGGCACCTTTGCCACACTGAGTGAAGTGCATGCTGCAAGCTGCACGTGGATCCT 314
QY 301 GAGAACTTCAGGCTCCTGGGCAACAGTGTGTGGTGTGTGTGGCCCATCATTGGCAAA 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
315 GAGAACTTCAGGCTCCTGGGCAACAGTGTGTGTGTGTGTGTGTGGCCCATCATTGGCAAA 374
QY 361 GAATTCACCCCAAGTATCAC 438
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
375 GAATTCACCCCAAGTATCAC 452
QY 421 CTGGCCCAAGTATCAC 438
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
435 CTGGCCCAAGTATCAC 452

RESULT 2
BU658312 515 bp mRNA linear EST 30-SEP-2002
LOCUS

DEFINITION cl34f02.z1 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo sapiens cDNA clone cl34f02 5', mRNA sequence.
ACCESSION BU658312
VERSION BU658312.1 GI:23370494
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 515)
AUTHORS Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
TITLE Gene Expression in Human Erythroid Precursor Cells
JOURNAL Unpublished
COMMENT Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD 20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jm7f@nih.gov
The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at:
http://hembase.niddk.nih.gov
Plate: 34 row: f column: 02
Seq primer: 5' lambda-TripleX2 Sequencing Primer.
Location/Qualifiers
1..515
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cl34f02"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl library)"
/note="Organ: blood; Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal
(N-terminal)-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC;
Http://www.nisc.nih.gov/)."

BASE COUNT 104 a 136 c 150 g 125 t

ORIGIN
Query Match 97.8%; Score 428.4; DB 13; Length 515;
Best Local Similarity 98.6%; Pred. No. 5.3e-103;
Matches 432; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GTGCACCTGACTCCTGAGGAGAGTGGCGCTTACTGCCCTGTGGGCAAGTGAACGTG 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
63 GTGCACCTGACTCCTGAGGAGAGTCTGCCGTACTGCCCTGTGGGCAAGTGAACGTG 122
QY 61 GATGAAGTTGGTGGTGGCCCTGGGCAAGGCTGCTGGTGGTCTACCTTGGACCCAGAGG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
123 GATGAAGTTGGTGGTGGCCCTGGGCAAGGCTGCTGGTGGTCTACCTTGGACCCAGAGG 182

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OM nucleic - nucleic search, using sw model
Run on: December 9, 2003, 15:17:59 ; Search time 290 Seconds
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Title: US-09-787-216A-2
Perfect score: 438
Sequence: 1 gtgcactgactcctgagga.....ccctggccacaagtatcac 438

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	428.4	97.8	625	10	US-09-782-378A-14
2	428.4	97.8	809	15	US-10-198-846-9489
3	425.2	97.1	438	9	US-09-839-164-3
4	425.2	97.1	438	14	US-10-085-853-32
5	425.2	97.1	438	15	US-10-128-581-22
6	422	96.3	1140	10	US-09-986-666-5
7	422	96.3	1140	10	US-09-986-666-7
8	422	96.3	1140	10	US-09-986-667-5
9	422	96.3	1140	10	US-09-986-667-7
10	422	96.3	1140	10	US-09-986-633-5
11	422	96.3	1140	10	US-09-986-633-7
12	420.4	96.0	743	13	US-10-280-679B-9
13	403.4	92.1	453	11	US-09-918-995-36836
14	393.2	89.8	468	10	US-09-880-107-2305
15	384.4	87.8	626	15	US-10-198-846-9446

16	376.4	85.9	431	11	US-09-918-995-18247	Sequence 18247, A
17	372.4	85.0	464	11	US-09-918-995-31979	Sequence 31979, A
18	362.6	82.8	415	11	US-09-918-995-16397	Sequence 16397, A
19	360.4	82.3	410	11	US-09-918-995-37115	Sequence 37115, A
20	357.2	81.6	407	11	US-09-918-995-16485	Sequence 16485, A
21	356.4	81.4	402	11	US-09-918-995-36558	Sequence 36558, A
22	356.4	81.4	402	11	US-09-918-995-36742	Sequence 36742, A
23	353.8	80.8	405	11	US-09-918-995-36878	Sequence 36878, A
24	353.2	80.6	589	13	US-09-882-945A-143	Sequence 143, App
25	352	80.4	407	11	US-09-918-995-36138	Sequence 36138, A
26	351.8	80.3	529	15	US-10-066-543-2089	Sequence 2089, Ap
27	351.4	80.2	411	11	US-09-918-995-36031	Sequence 36031, A
28	342.8	78.3	400	11	US-09-918-995-18083	Sequence 18083, A
29	326	74.4	365	11	US-09-918-995-30136	Sequence 30136, A
30	313.4	71.6	902	15	US-10-198-846-6717	Sequence 6717, Ap
31	310	70.8	613	10	US-09-147-490-6	Sequence 6, Appli
32	310	70.8	613	10	US-09-147-490-7	Sequence 7, Appli
33	310	70.8	620	10	US-09-147-490-9	Sequence 9, Appli
34	305.4	69.7	345	11	US-09-918-995-18654	Sequence 18654, A
35	304	69.4	412	11	US-09-918-995-36372	Sequence 36372, A
36	300	68.5	347	11	US-09-918-995-18044	Sequence 18044, A
37	296.2	67.6	397	11	US-09-918-995-36918	Sequence 36918, A
38	290.8	66.4	368	11	US-09-918-995-19075	Sequence 19075, A
39	284.4	64.9	343	11	US-09-918-995-18967	Sequence 18967, A
40	272.6	62.2	339	11	US-09-918-995-18150	Sequence 18150, A
41	263.8	60.2	575	14	US-10-044-090-262	Sequence 262, App
42	256.8	58.6	481	11	US-09-918-995-32565	Sequence 32565, A
43	250.6	57.2	424	13	US-09-814-353-17210	Sequence 17210, A
44	239	54.6	919	13	US-09-814-353-21253	Sequence 21253, A
45	233.4	53.3	562	13	US-10-393-602-122	Sequence 122, App

ALIGNMENTS

RESULT 1
US-09-782-378A-14
; Sequence 14, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-378A-14

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Best Local Similarity		98.6%	Pred. No. 1.6e-123;		
Matches 432;		Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	GTGCACCTGACTCCTGAGGAGGAGTGGCCGTTACTGCTCCCTGTGGGGCAAGTGAACGTG	60		
Db	54	GTGCACCTGACTCCTGAGGAGAGTGTCCGTTACTGCTCCCTGTGGGGCAAGTGAACGTG	113		
QY	61	GATGAAGTTGGTGGTGGCCCTGGGAGGCTGTGGTGGTCTACCTTGGACCCAGAGG	120		
Db	114	GATGAAGTTGGTGGTGGCCCTGGGAGGCTGTGGTGGTCTACCTTGGACCCAGAGG	173		
QY	121	TTCTTTGAGTCTTTGGGATCTGTCCACTCTCTGATCTGTATGGCAACCTAAGGTG	180		
Db	174	TTCTTTGAGTCTTTGGGATCTGTCCACTCTCTGATCTGTATGGCAACCTAAGGTG	233		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2003, 14:24:49 ; Search time 64 Seconds
(without alignments)
3020.716 Million cell updates/sec

Title: US-09-787-216A-2
Perfect score: 438
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	428.4	97.8	438	1 US-08-170-095B-4	Sequence 4, Appli
2	428.4	97.8	438	1 US-08-396-866-4	Sequence 4, Appli
3	428.4	97.8	438	1 US-08-484-686B-6	Sequence 6, Appli
4	428.4	97.8	438	3 US-08-381-175A-4	Sequence 4, Appli
5	428.4	97.8	438	3 US-08-463-160B-6	Sequence 6, Appli
6	428.4	97.8	438	3 US-09-031-361-4	Sequence 4, Appli
7	425.2	97.1	438	2 US-08-627-173-17	Sequence 17, Appl
8	425.2	97.1	438	2 US-08-535-882A-17	Sequence 17, Appl
9	425.2	97.1	438	3 US-08-316-424A-3	Sequence 3, Appli
10	425.2	97.1	438	3 US-09-005-546-17	Sequence 17, Appl
11	425.2	97.1	438	4 US-08-983-564A-32	Sequence 32, Appl
12	425.2	97.1	438	4 US-08-477-669-3	Sequence 3, Appli
13	423.6	96.7	444	2 US-08-432-071B-3	Sequence 3, Appli
14	423.6	96.7	743	3 US-08-483-502-9	Sequence 9, Appli
15	423.6	96.7	743	4 US-09-726-651A-9	Sequence 9, Appli
16	422	96.3	1140	4 US-09-598-218-5	Sequence 5, Appli
17	422	96.3	1140	4 US-09-598-218-7	Sequence 7, Appli
18	420.4	96.0	743	1 US-07-923-692C-9	Sequence 9, Appli
19	420.4	96.0	743	1 US-08-184-237-9	Sequence 9, Appli
20	420.4	96.0	743	2 US-08-482-920-9	Sequence 9, Appli
21	420.4	96.0	743	3 US-08-484-341-9	Sequence 9, Appli
22	374.6	85.5	438	1 US-08-484-686B-4	Sequence 4, Appli
23	374.6	85.5	438	3 US-08-463-160B-4	Sequence 4, Appli
24	288.2	65.8	1460	3 US-09-058-562-1	Sequence 1, Appli
25	286.6	65.4	438	3 US-08-381-175A-6	Sequence 6, Appli
26	286.6	65.4	1464	1 US-08-240-712-1	Sequence 1, Appli
27	286.6	65.4	1464	1 US-08-443-890-1	Sequence 1, Appli

28	286.6	65.4	1464	5 PCT-US92-09752-1	Sequence 1, Appli
29	281.2	64.2	438	1 US-08-484-686B-2	Sequence 2, Appli
30	281.2	64.2	438	3 US-08-463-160B-2	Sequence 2, Appli
31	262.2	59.9	438	1 US-08-484-686B-3	Sequence 3, Appli
32	262.2	59.9	438	3 US-08-463-160B-3	Sequence 3, Appli
33	262.2	59.9	534	1 US-08-484-686B-10	Sequence 10, Appl
34	262.2	59.9	534	3 US-08-463-160B-10	Sequence 10, Appl
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36	251.8	57.5	443	1 US-08-374-144-4	Sequence 4, Appli
37	251.8	57.5	443	1 US-08-775-164-4	Sequence 4, Appli
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40	251.8	57.5	443	5 PCT-US93-06828-4	Sequence 4, Appli
41	233.4	53.3	562	1 US-08-592-126-122	Sequence 122, App
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43	220.6	50.4	600	5 PCT-US96-09430-15	Sequence 15, Appl
C 44	220.6	50.4	1666	1 US-08-076-090-1	Sequence 1, Appli
C 45	220.6	50.4	1666	5 PCT-US94-06661-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-170-095B-4
; Sequence 4, Application US/08170095B
; Patent No. 5563254
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen J.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Blood Substitutes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,095B
; FILING DATE: December 20, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5563254ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: Hoffman 2A/CONT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown to applicant
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Human beta globin sequence
; HYPOTHETICAL: no
US-08-170-095B-4

Query Match 97.8%; Score 428.4; DB 1; Length 438;
Best Local Similarity 98.6%; Pred. No. 4.1e-110;
Matches 432; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Db 1 GTGCACCTGACTCCTGAGGAGGAGTGGCGTACTGCGCCCTGTGGGGCAAGTGACCTG 60

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QY	421	CTGGCCCCACAAGTATCAC	438
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RESULT 2
US-08-396-866-4
; Sequence 4, Application US/08396866
; Patent No. 561124
; GENERAL INFORMATION:
; APPLICANT: Hoffman, Stephen J.
; APPLICANT: Nagai, Kiyoshi
; TITLE OF INVENTION: Blood Substitutes
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

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US-08-396-866-4
Query Match          97.8%; Score 428.4; DB 1; Length 438;
Best Local Similarity 98.6%; Pred. No. 4.1e-110;
Matches 432; Conservative 0; Mismatches 6; Indels 0; Gaps 0

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Qy     61 GATGAAGTTGGTGGTAGGSCCTGGGCAGGCTGCTGGTGTCACCCCTTGGACCCAGAG 120
        |||
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Db    121 TTCTTTGAGTCCTTTGGGGATCTGTCCACTCCTGATGCTGTATTGGGCAACCCTAAGGTG 180

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Qy    241 CTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCATGCTGACAAGCTGCAACGTGGATCCT 300
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Db    241 CTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCATGCTGACAAGCTGCAACGTGGATCCT 300

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Qy    361 GAATTCACCCOACCAAGTGCAAGGCTGCCTATCAGAAAAGTGGTGGGTGGCTTAATGCC 420
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RESULT 3
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 ; Sequence 6, Application US/08484686B
 ; Patent No. 5827693
 ; GENERAL INFORMATION:
 ; APPLICANT: De Angelo, Joseph
 ; APPLICANT: Motwani, Nalini
 ; APPLICANT: Bajwa, Wajeeh
 ; TITLE OF INVENTION: Expression of Recombinant Hemoglobin and
 ; TITLE OF INVENTION: Hemoglobin Variants in Yeast
 ; NUMBER OF SEQUENCES: 71
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,686B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/368,407
 ; FILING DATE: 29-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/876,290
 ; FILING DATE: 29-APR-1992
 ; PRIOR APPLICATION DATA:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2003, 14:17:18 ; Search time 279 Seconds
(without alignments)
4237.827 Million cell updates/sec

Title: US-09-787-216A-2
Perfect score: 438
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Scoring table: IDENTITY_NUC
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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	438	100.0	438	21	DNA encoding human
2	428.4	97.8	438	22	Human hemoglobin a
3	428.4	97.8	625	24	Human beta chain o
4	428.4	97.8	634	13	Encodes mutated hu
5	425.2	97.1	438	14	Beta-globin coding
6	425.2	97.1	438	17	Human beta haemogl
7	425.2	97.1	438	18	cDNA encoding the
8	425.2	97.1	626	15	Human beta globin

9	422	96.3	438	14	AAQ46965	Human adult beta h
10	422	96.3	1140	24	AAQ28588	Human alpha and be
11	422	96.3	1140	24	AAQ28590	Human alpha and be
12	420.4	96.0	699	13	AAQ20236	Encodes human beta
13	420.4	96.0	743	14	AAQ37682	Encodes human beta
14	420.4	96.0	743	15	AAQ65576	Petunia EFSP synth
15	420.4	96.0	743	18	AAQ47097	Beta-haemoglobin +
16	420.4	96.0	743	18	AAQ61375	Beta-haemoglobin c
17	420.4	96.0	743	20	AAQ29146	Human beta-haemogl
18	420.4	96.0	743	20	AAQ03388	DNA sequence encod
19	420.4	96.0	743	21	AAQ12396	Human beta-hemoglo
20	417.8	95.4	438	9	AAQ80526	Mutant beta-globin
21	412.8	94.2	696	13	AAQ20237	Encodes Val(1) to
22	393.2	89.8	468	24	ABT10908	Human breast cance
23	393.2	89.8	468	24	ABK83969	Human cDNA differe
24	393.2	89.8	468	24	ABN95807	Gene #2305 used to
25	393.2	89.8	468	24	ABL68603	Kidney cancer rela
26	382.8	87.4	627	22	AAK52383	Human polynucleoti
27	376.8	86.0	475	24	ABQ93519	Human cDNA SEQ ID
28	375.8	85.5	592	22	AAQ44651	Human full-length
29	374.6	85.5	438	22	AAF31394	Human hemoglobin a
30	371.4	84.8	438	14	AAQ46963	Human adult delta
31	354.8	81.0	589	15	AAQ55626	Rabbit beta globin
32	353.2	80.6	589	24	ABL46176	Rabbit beta-globin
33	350.4	80.0	454	21	AAQ01758	Human secreted pro
34	347.2	79.3	498	24	ABL56589	Nucleotide sequenc
35	310	70.8	613	19	AAV03044	Rat EX clone nucle
36	295	67.4	366	22	AAI82469	Human polynucleoti
37	290.8	66.4	368	22	AAQ44823	Human contig polyn
38	286.6	65.4	1464	14	AAQ42395	(Des-Val)-alpha-(G
39	285	65.1	1463	11	AAQ06685	Polycistronic oper
40	281.2	64.2	438	22	AAF31392	Human hemoglobin e
41	281.2	64.2	618	22	AAF27743	Human transport pr
42	279.6	63.8	438	14	AAQ46961	Human embryonic ep
43	278	63.5	1065	11	AAQ06684	Polycistronic oper
44	277.2	63.3	896	24	ABQ66961	Human haemoglobin
45	263.8	60.2	575	25	ABX63262	Human cDNA #262 di

ALIGNMENTS

RESULT 1
AAZ94729
ID AAZ94729 standard; DNA; 438 BP.
XX
AC AAZ94729;
XX
DT 01-AUG-2000 (first entry)
XX
DE DNA encoding human mutant beta-globin.
XX
KW Beta-globin; haemoglobin; Hb Prisca; human; mutant;
KW blood substitute; antianemic; oxygen-carrier; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200018802-A1.
XX
PD 06-APR-2000.
XX
PF 30-SEP-1999; 99WO-US22756.
XX
PR 01-OCT-1998; 98US-0102640.
XX
PA (UTEM) UNIV TEMPLE.
XX
PI Fronticelli C;
XX
DR WPI; 2000-293112/25.
DR P-PSDB; AAY79378.
XX

PT Mutant human beta-globin polypeptides used for generating a blood substitute to supplement the oxygen-carrying capacity of a patient's blood comprises substitution or deletion of native cysteine residues -

xx
PS
Claim 6: Page 34-35; 42pp; English.

The present sequence is that of DNA encoding a mutant human beta-globin (see AAY9378) in which the native Ser-9 residue of human beta-globin is substituted by Cys, native Cys-93 is substituted by Ala, and native Cys-112 is substituted by Gly. A haemoglobin comprising the mutant beta-globin and normal alpha-globin is termed Hb-Prisca and is characterised as having high oxygen carrying capacity but low oncotic pressure, making it a useful blood substitute. Since the tetrameric haemoglobin molecule Hb prisca contains 2 beta-globin molecules and 2 alpha-globin molecules, the 3-position mutation results in a total of 6 mutations per tetramer. These mutations allow for proper folding of the recombinant product and increased yield. The mutant tetramers (64 kDa) equilibrate to form a homogeneous haemoglobin polymer of 7 tetramers (450 kDa). Vectors and transformed host cells for producing the beta-globin mutants are provided.

Sequence 438 BP: 85 A: 114 C: 137 G: 102 T: 0 other;

Query Match	100.0%;	Score 438;	DB 21;	Length 438;
Best Local Similarity	100.0%;	Pred. No. 3.3e-105;		
Matches 438; Conservative	0;	Mismatches	0;	Indels

QY	1	GTGCACCTGACTCCTGAGGAGAAAGTGGCCCGTTACTGCCCTGTGGGCAAGGTGAACGTG	60
Db	1	GTGCACCTGACTCCTGAGGAGAAAGTGGCCCGTTACTGCCCTGTGGGCAAGGTGAACGTG	60
QY	61	GATGAAGTTGGTGTGAGGCCCTTGGCAGGCTGCTGGTGGTCTACCTTGGACCCAGAGG	120
Db	61	GATGAAGTTGGTGTGAGGCCCTTGGCAGGCTGCTGGTGGTCTACCTTGGACCCAGAGG	120
QY	121	TTCTTTGAGTCCCTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGCAACCCCTAAGTGT	180
Db	121	TTCTTTGAGTCCCTTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGCAACCCCTAAGTGT	180
QY	181	AAGGCTCATGGCAAGAAAGTGTCTCGGTGCTTTAGTGATGGCCTGGCTCACCTGGACAAC	240
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QY	241	CTCAAGGGCACCTTTGGCCACACTGAGTGAGCTGCATGCTGACAAAGCTGCACGTGGATCCT	300
Db	241	CTCAAGGGCACCTTTGGCCACACTGAGTGAGCTGCATGCTGACAAAGCTGCACGTGGATCCT	300
QY	301	GAGAACTTCAGGCTCCTGGGCAACGTCGTGGTGGTGGTGGCCCATCACCTTTGGCAAA	360
Db	301	GAGAACTTCAGGCTCCTGGGCAACGTCGTGGTGGTGGTGGCCCATCACCTTTGGCAAA	360
QY	361	GAATTACCCCAACAGTGAGGCTGCCCTATCAGAAAGTGGTGGCTGGTGGCTAATGCC	420
Db	361	GAATTACCCCAACAGTGAGGCTGCCCTATCAGAAAGTGGTGGCTGGTGGCTAATGCC	420
QY	421	CTGGCCCAACAAGTATCAC	438
Db	421	CTGGCCCAACAAGTATCAC	438

RESULT 2
AAAF31396
ID AAAF31396 standard: DNA: 438 BP.

AA
AC AAF31396:

XX DT 10-APR-2001 (first entry)

Human hemoglobin adult beta DNA.

Hemoglobin: globin; oxygen carrier; ds.

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OS	Homo sapiens.
XX	
PN	US6172039-B1.
XX	
PD	09-JAN-2001.
XX	
PF	05-JUN-1995; 95US-0463160.
XX	
PR	29-DEC-1994; 94US-0368407.
PR	07-JUN-1995; 95US-0484686.
PR	29-APR-1992; 92US-0876290.
PR	16-APR-1990; 90US-0509918.
PR	14-NOV-1990; 90US-0614359.
PR	12-APR-1991; 91US-0684611.
XX	
PA	(APEX-) APEX BIOSCIENCE INC.

De Angelo J, Motwani NM, Bajwa W, Bonaventura J;
WPI: 2001-136882/14.

Novel globin chain in combination with a source of heme useful for producing hemoglobin, is free of erythrocyte membrane component, mammalian cell components and *Escherichia coli* endotoxins

XX PS Disclosure: Fig 1; 144pp; English.

The present invention relates to a substantially pure globin chain which is free of erythrocyte membrane components, *Escherichia coli* endotoxins and mammalian cell components. The globin combined with a source of heme is useful for producing hemoglobin, which in turn is useful as physiological oxygen carrier in blood substitute solutions and in plasma expanders or in applications requiring a physiological oxygen carrier.

Sequence 438 BP; 85 A; 114 C; 135 G; 104 T; 0 other;
XX
SO

Query Match 97.8%; Score 428.4; DB 22; Length 438;
Best Local Similarity 98.6%; Pred. No. 1.1e-102;
Matches 432: Conservative 0; Mismatches 6; Indels 0;

QY	1	GTGCACCTGACTCCTGAGGAGAAGTGGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG	60
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QY	121	TTCTTTGAGTCCCTTGGGGATCTGTCCACTCCTGATGCTGTTATGGGGCAACCCCTAAGGTG	180
Db	121		180
QY	181	AAGGCTCATGGCAAGAAAGTGCTCGGTGCCCTTTAGTGATGGCCTGGCTCACCTGGACAAC	240
Db	181		240
QY	241	CTCAAGGGCACCTTTGCCACACTGAGTGAGCTGCGTGTGATGCTGACAAAGCTGCACGTGGATCCT	300
Db	241		300
QY	301	GAGAACTTCAGGTCTCTGGGCAACGTGCTGTCGGTGTGCTGCGCCCATCACCTTTGGCAAA	360
Db	301		360
QY	361	GAATTCACCCCAACAGTGACGGTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCC	420
Db	361		420
QY	421	CTGGCCCCACAAGTATCAC	438
Db	421		438